

SEQUENCE LISTING

<110> Reed, John C.
Zapata, Juan M.

<120> Novel TRAF Family Proteins

<130> P-LJ 4453

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<150> US 09/434,784

<151> 1999-11-05

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<170> PatentIn Ver. 2.0

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Met Asn His Gln Gln Gln Gln Gln Gln Lys

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gcg ggc gag cag cag ttg agc gag ccc gag gac atg gag atg gaa gcg 280

Ala Gly Glu Gln Gln Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala

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gga gat aca gat gac cca cca aga att act cag aac cct gtg atc aat 328

Gly Asp Thr Asp Asp Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn

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Gly Asn Val Ala Leu Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met
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 Glu Asp Asp Thr Ser Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val
 60 65 70 75

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 Glu Arg Phe Ser Arg Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe
 80 85 90

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 Val Arg Asn Leu Pro Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro
 95 100 105

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 Asp Arg Pro His Gln Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala
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 Glu Ser Asp Ser Thr Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys
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 Ile Ile Asn Tyr Arg Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser
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 His Leu Phe Phe His Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met
 160 165 170

gcc tgg agt gaa gtg acc gat cct gag aaa gga ttt ata gat gat gac 760
 Ala Trp Ser Glu Val Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp
 175 180 185

aaa gtt acc ttt gaa gtc ttt gta cag gcg gat gct ccc cat gga gtt 808
 Lys Val Thr Phe Glu Val Phe Val Gln Ala Asp Ala Pro His Gly Val
 190 195 200

gcg tgg gat tca aag aag cac aca ggc tac gtc ggc tta aag aat cag 856
 Ala Trp Asp Ser Lys Lys His Thr Gly Tyr Val Gly Leu Lys Asn Gln
 205 210 215

gga gcg act tgt tac atg aac agc ctg cta cag acg tta ttt ttc acg 904
 Gly Ala Thr Cys Tyr Met Asn Ser Leu Leu Gln Thr Leu Phe Phe Thr
 220 225 230 235

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Cys	Arg	Val	Leu	Leu	Asp	Asn	Val	Glu	Asn	Lys	Met	Lys	Gly	Thr	Cys	
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Tyr	Asp	Ile	Gln	Leu	Ser	Ile	Lys	Gly	Lys	Lys	Asn	Ile	Phe	Glu	Ser	
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Phe	Val	Asp	Tyr	Val	Ala	Val	Glu	Gln	Leu	Asp	Gly	Asp	Asn	Lys	Tyr	
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Asp	Ala	Gly	Glu	His	Gly	Leu	Gln	Glu	Ala	Glu	Lys	Gly	Val	Lys	Phe	
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Asp	Pro	Gln	Thr	Asp	Gln	Asn	Ile	Lys	Ile	Asn	Asp	Arg	Phe	Glu	Phe	
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Ala Met Leu Asp Asn Glu Ala Asp Gly Asn Lys Thr Met Ile Glu Leu	
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agt gat aat gaa aac cct tgg aca ata ttc ctg gaa aca gtt gat ccc	2200
Ser Asp Asn Glu Asn Pro Trp Thr Ile Phe Leu Glu Thr Val Asp Pro	
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Glu Leu Ala Ala Ser Gly Ala Thr Leu Pro Lys Phe Asp Lys Asp His	
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Asp Val Met Leu Phe Leu Lys Met Tyr Asp Pro Lys Thr Arg Ser Leu	
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gac atc ata gta ttt cag aag gat gac cct gaa aat gat aac agt gaa	2536
Asp Ile Ile Val Phe Gln Lys Asp Asp Pro Glu Asn Asp Asn Ser Glu	
765 770 775	
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Leu Pro Thr Ala Lys Glu Tyr Phe Arg Asp Leu Tyr His Arg Val Asp	
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Val Ile Phe Cys Asp Lys Thr Ile Pro Asn Asp Pro Gly Phe Val Val	
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acg tta tca aat aga atg aat tat ttt cag gtt gca aag aca gtt gca	2680

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Asp	Glu	Leu	Leu	Glu	Cys	Leu	Ser	Pro	Ala	Thr	Ser	Arg	Thr	Phe	Arg		
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 Val Met Lys Arg Ile Gln Ser Leu Leu Asp Ile Gln Glu Lys Glu Phe
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 Glu Lys Phe Lys Phe Ala Ile Val Met Thr Gly Arg His Gln Tyr Ile
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aat gaa gac gag tat gaa gta aat ttg aaa gac ttt gag cca cag ccc 3400
 Asn Glu Asp Glu Tyr Glu Val Asn Leu Lys Asp Phe Glu Pro Gln Pro
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ggt aat atg tct cat cct cgg cct tgg cta ggg ctc gac cac ttc aac 3448
 Gly Asn Met Ser His Pro Arg Pro Trp Leu Gly Leu Asp His Phe Asn
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aaa gcc cca aag agg agt cgc tac act tac ctt gaa aag gcc att aaa 3496
 Lys Ala Pro Lys Arg Ser Arg Tyr Thr Tyr Leu Glu Lys Ala Ile Lys
 1085 1090 1095

atc cat aac tgattttccaa gctggtgtgt tcaaggcgag gacggtgtgt 3545
 Ile His Asn
 1100

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Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser
50 55 60

Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg
65 70 75 80

Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro
85 90 95

Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln
100 105 110

Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr
115 120 125

Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg
130 135 140

Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His
145 150 155 160

Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val
165 170 175

Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu
180 185 190

Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys
195 200 205

Lys His Thr Gly Tyr Val Gly Leu Lys Asn Gln Gly Ala Thr Cys Tyr
210 215 220

Met Asn Ser Leu Leu Gln Thr Leu Phe Phe Thr Asn Gln Leu Arg Lys
225 230 235 240

Ala Val Tyr Met Met Pro Thr Glu Gly Asp Asp Ser Ser Lys Ser Val

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Pro Val Gly Thr Lys Lys Leu Thr Lys Ser Phe Gly Trp Glu Thr Leu		
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Asp Ser Phe Met Gln His Asp Val Gln Glu Leu Cys Arg Val Leu Leu		
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Asp Asn Val Glu Asn Lys Met Lys Gly Thr Cys Val Glu Gly Thr Ile		
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Pro Lys Leu Phe Arg Gly Lys Met Val Ser Tyr Ile Gln Cys Lys Glu		
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Val Asp Tyr Arg Ser Asp Arg Arg Glu Asp Tyr Tyr Asp Ile Gln Leu		
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Ser Ile Lys Gly Lys Lys Asn Ile Phe Glu Ser Phe Val Asp Tyr Val		
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Ala Val Glu Gln Leu Asp Gly Asp Asn Lys Tyr Asp Ala Gly Glu His		
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Gly Leu Gln Glu Ala Glu Lys Gly Val Lys Phe Leu Thr Leu Pro Pro		
385	390	395 400
Val Leu His Leu Gln Leu Met Arg Phe Met Tyr Asp Pro Gln Thr Asp		
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Gln Asn Ile Lys Ile Asn Asp Arg Phe Glu Phe Pro Glu Gln Leu Pro		
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Leu Asp Glu Phe Leu Gln Lys Thr Asp Pro Lys Asp Pro Ala Asn Tyr		
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Ile Leu His Ala Val Leu Val His Ser Gly Asp Asn His Gly Gly His		
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Tyr Val Val Tyr Leu Asn Pro Lys Gly Asp Gly Lys Trp Cys Lys Phe		
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Asn Tyr Gly Gly His Asp Asp Asp Leu Ser Val Arg His Cys Thr Asn		

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Ala His Leu Tyr Met Gln Val Gln Ile Val Ala Glu Asp Gln Phe Cys		
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625	630	635
Glu Ala Asp Gly Asn Lys Thr Met Ile Glu Leu Ser Asp Asn Glu Asn		
645	650	655
Pro Trp Thr Ile Phe Leu Glu Thr Val Asp Pro Glu Leu Ala Ala Ser		
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Gly Ala Thr Leu Pro Lys Phe Asp Lys Asp His Asp Val Met Leu Phe		
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Leu Lys Met Tyr Asp Pro Lys Thr Arg Ser Leu Asn Tyr Cys Gly His		
690	695	700
Ile Tyr Thr Pro Ile Ser Cys Lys Ile Arg Asp Leu Leu Pro Val Met		
705	710	715
Cys Asp Arg Ala Gly Phe Ile Gln Asp Thr Ser Leu Ile Leu Tyr Glu		
725	730	735
Glu Val Lys Pro Asn Leu Thr Glu Arg Ile Gln Asp Tyr Asp Val Ser		
740	745	750
Leu Asp Lys Ala Leu Asp Glu Leu Met Asp Gly Asp Ile Ile Val Phe		

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Glu Val Asn Leu Lys Asp Phe Glu Pro Gln Pro Gly Asn Met Ser His		
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 Met Ser Arg Val Pro Ser
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cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223
 Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp
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 Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile
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 Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser
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gta	aac	ccc	aaa	ggg	tta	gat	gaa	gaa	agc	aaa	gat	tac	ctg	tca	ctt	415
Val	Asn	Pro	Lys	Gly	Leu	Asp	Glu	Glu	Ser	Lys	Asp	Tyr	Leu	Ser	Leu	
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tac	ctg	tta	ctg	gtc	agc	tgt	cca	aag	agt	gaa	gtt	cgg	gca	aaa	ttc	463
Tyr	Leu	Leu	Leu	Val	Ser	Cys	Pro	Lys	Ser	Glu	Val	Arg	Ala	Lys	Phe	
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Lys	Phe	Ser	Ile	Leu	Asn	Ala	Lys	Gly	Glu	Glu	Thr	Lys	Ala	Met	Glu	
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Ser	Gln	Arg	Ala	Tyr	Arg	Phe	Val	Gln	Gly	Lys	Asp	Trp	Gly	Phe	Lys	
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Lys	Phe	Ile	Arg	Arg	Asp	Phe	Leu	Leu	Asp	Glu	Ala	Asn	Gly	Leu	Leu	
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Glu	Cys	Arg	Leu	Ala	Asp	Glu	Leu	Gly	Gly	Leu	Trp	Glu	Asn	Ser	Arg	
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Phe	Thr	Asp	Cys	Cys	Leu	Cys	Val	Ala	Gly	Gln	Glu	Phe	Gln	Ala	His	
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Lys	Ala	Ile	Leu	Ala	Ala	Arg	Ser	Pro	Val	Phe	Ser	Ala	Met	Phe	Glu	
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His	Glu	Met	Glu	Glu	Ser	Lys	Lys	Asn	Arg	Val	Glu	Ile	Asn	Asp	Val	
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Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Asp	
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Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys	
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Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp	
295 300 305 310	
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Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn	
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tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg	1183
Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val	
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Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser	
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Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
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Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
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Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
85 90 95

Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
100 105 110

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
115 120 125

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
130 135 140

Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
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Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
165 170 175

Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
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Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
195 200 205

Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
210 215 220

Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg

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Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
245 250 255

Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp
260 265 270

Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
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Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
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Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
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Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
325 330 335

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Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val Phe Arg Cys Phe Ile
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Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser Lys	
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Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val Asn	
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Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln Leu	
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Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu Asn	
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cac cat gaa aaa ctt agt gta ttt tgc tgg act tgt aag aag tgt atc	384
His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys Ile	
115 120 125	
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Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr Phe	
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Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn Glu	
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Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys Thr	
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Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys Ser	
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Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met Ala	
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Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr Leu	
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Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys Asn	
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Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg Phe	
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Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His Trp	
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Tyr Ile Thr Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln Ile	
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Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met Leu	
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565 570 575	
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Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu Asp	
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Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg Pro	
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Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val Asn
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His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys Ile
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Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr Phe
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Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys Ser
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Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met Ala
260 265 270

Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu Val

275 280 285
 Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr Leu
 290 295 300
 Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser Gly
 305 310 315 320
 Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val Arg
 325 330 335
 Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro Glu
 340 345 350
 Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys Asn
 355 360 365
 Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp Phe Glu Val
 370 375 380
 Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu Ala
 385 390 395 400
 Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg Phe
 405 410 415
 Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His Trp
 420 425 430
 Tyr Ile Thr Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln Ile
 435 440 445
 Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln Lys
 450 455 460
 Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn Asp
 465 470 475 480
 Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met Leu
 485 490 495
 Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu Asp
 500 505 510
 Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu Leu
 515 520 525
 Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val Asn

530		535		540	
Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser Asn					
545		550		555	560
Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn Asp					
	565		570		575
Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu Asp					
	580		585		590
Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly Ser					
	595		600		605
Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr Ser					
	610		615		620
Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp Leu					
	625		630		635
Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg Pro					
		645		650	655
Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp Lys					
	660		665		670
Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu Lys					
	675		680		685
Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met Lys					
	690		695		700
Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala Ala					
	705		710		715
Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala Leu					
		725		730	735
Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly Met					
	740		745		750
Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn Ser					
	755		760		765
Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val Ala					
	770		775		780
Gly Ser Leu Ser Leu Arg Arg Ala Val Asp Pro Gly Glu Asn Ser Arg					

785 790 795 800
 Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser Ser
 805 810 815
 Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly Ser
 820 825 830
 Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala Leu
 835 840 845
 Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala Val
 850 855 860
 Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly Gly
 865 870 875 880
 His Leu Glu Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu Thr
 885 890 895
 Gly Glu Leu Gln Pro Val Leu Pro Glu Gly Ala Ser Ala Ala Pro Glu
 900 905 910
 Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys Asp Thr Glu Asn Glu
 915 920 925
 Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe Met
 930 935 940
 Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Phe Pro Asp
 945 950 955 960
 Gly Glu Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu Asn
 965 970 975
 Ser Gly Arg

<210> 7
 <211> 639
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(639)

<400> 7

atg aac cac cag cag cag cag cag cag cag cag aaa gcg ggc gag cag cag	48
Met Asn His Gln Gln Gln Gln Gln Gln Gln Lys Ala Gly Glu Gln Gln	
1 5 10 15	
ttg agc gag ccc gag gac atg gag atg gaa gcg gga gat aca gat gac	96
Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala Gly Asp Thr Asp Asp	
20 25 30	
cca cca aga att act cag aac cct gtg atc aat ggg aat gtg gcc ctg	144
Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn Gly Asn Val Ala Leu	
35 40 45	
agt gat gga cac aac acc gcg gag gag gac atg gag gat gac acc agt	192
Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser	
50 55 60	
tgg cgc tcc gag gca acc ttt cag ttc act gtg gag cgc ttc agc aga	240
Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg	
65 70 75 80	
ctg agt gag tcg gtc ctt agc cct ccg tgt ttt gtg cga aat ctg cca	288
Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro	
85 90 95	
tgg aag att atg gtg atg cca cgc ttt tat cca gac aga cca cac caa	336
Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln	
100 105 110	
aaa agc gta gga ttc ttt ctc cag tgc aat gct gaa tct gat tcc acg	384
Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr	
115 120 125	
tca tgg tct tgc cat gca caa gca gtg ctg aag ata ata aat tac aga	432
Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg	
130 135 140	
gat gat gaa aag tcg ttc agt cgt cgt att agt cat ttg ttc ttc cat	480
Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His	
145 150 155 160	
aaa gaa aat gat tgg gga ttt tcc aat ttt atg gcc tgg agt gaa gtg	528
Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val	
165 170 175	
acc gat cct gag aaa gga ttt ata gat gat gac aaa gtt acc ttt gaa	576
Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu	
180 185 190	

gtc ttt gta cag gcg gat gct ccc cat gga gtt gcg tgg gat tca aag 624
 Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys
 195 200 205

aag cac aca ggc tac 639
 Lys His Thr Gly Tyr
 210

<210> 8
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Asn His Gln Gln Gln Gln Gln Gln Lys Ala Gly Glu Gln Gln
 1 5 10 15

Leu Ser Glu Pro Glu Asp Met Glu Met Glu Ala Gly Asp Thr Asp Asp
 20 25 30

Pro Pro Arg Ile Thr Gln Asn Pro Val Ile Asn Gly Asn Val Ala Leu
 35 40 45

Ser Asp Gly His Asn Thr Ala Glu Glu Asp Met Glu Asp Asp Thr Ser
 50 55 60

Trp Arg Ser Glu Ala Thr Phe Gln Phe Thr Val Glu Arg Phe Ser Arg
 65 70 75 80

Leu Ser Glu Ser Val Leu Ser Pro Pro Cys Phe Val Arg Asn Leu Pro
 85 90 95

Trp Lys Ile Met Val Met Pro Arg Phe Tyr Pro Asp Arg Pro His Gln
 100 105 110

Lys Ser Val Gly Phe Phe Leu Gln Cys Asn Ala Glu Ser Asp Ser Thr
 115 120 125

Ser Trp Ser Cys His Ala Gln Ala Val Leu Lys Ile Ile Asn Tyr Arg
 130 135 140

Asp Asp Glu Lys Ser Phe Ser Arg Arg Ile Ser His Leu Phe Phe His
 145 150 155 160

Lys Glu Asn Asp Trp Gly Phe Ser Asn Phe Met Ala Trp Ser Glu Val
 165 170 175

Thr Asp Pro Glu Lys Gly Phe Ile Asp Asp Asp Lys Val Thr Phe Glu
 180 185 190

Val Phe Val Gln Ala Asp Ala Pro His Gly Val Ala Trp Asp Ser Lys
 195 200 205

Lys His Thr Gly Tyr
 210

<210> 9

<211> 540

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(540)

<400> 9

atg tca agg gtt cca agt cct cca cct ccg gca gaa atg tcg agt ggc 48
 Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly
 1 5 10 15

ccc gta gct gag agt tgg tgc tac aca cag atc aag gta gtg aaa ttc 96
 Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe
 20 25 30

tcc tac atg tgg acc atc aat aac ttt agc ttt tgc cgg gag gaa atg 144
 Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met
 35 40 45

ggc gaa gtc att aaa agt tct aca ttt tca tca gga gca aat gat aaa 192
 Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
 50 55 60

ctg aaa tgg tgt ttg cga gta aac ccc aaa ggg tta gat gaa gaa agc 240
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
 65 70 75 80

aaa gat tac ctg tca ctt tac ctg tta ctg gtc agc tgt cca aag agt 288
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
 85 90 95

gaa gtt cgg gca aaa ttc aaa ttc tcc atc ctg aat gcc aag gga gaa 336
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
 100 105 110

gaa acc aaa gct atg gag agt caa cgg gca tat agg ttt gtg caa ggc 384
 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
 115 120 125

aaa gac tgg gga ttc aag aaa ttc atc cgt aga gat ttt ctt ttg gat 432
 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
 130 135 140

gag gcc aac ggg ctt ctc cct gat gac aag ctt acc ctc ttc tgc gag 480
 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
 145 150 155 160

gtg agt gtt gtg caa gat tct gtc aac att tct ggc cag aat acc atg 528
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
 165 170 175

aac atg gta aag 540
 Asn Met Val Lys
 180

<210> 10
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly
 1 5 10 15
 Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe
 20 25 30
 Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met
 35 40 45
 Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
 50 55 60
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
 65 70 75 80
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
 85 90 95
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
 100 105 110

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
 115 120 125

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
 130 135 140

Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
 145 150 155 160

Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
 165 170 175

Asn Met Val Lys
 180

<210> 11

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(459)

<400> 11

ttt acc agt gaa tta gtg cca tct tac gat tca gct act ttt gtt tta 48
 Phe Thr Ser Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu
 1 5 10 15

gag aat ttc agc act ttg cgt cag aga gca gat cct gtt tac agt cca 96
 Glu Asn Phe Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro
 20 25 30

cct ctt caa gtt tca gga ctt tgc tgg agg tta aaa gtt tac cca gat 144
 Pro Leu Gln Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp
 35 40 45

gga aat gga gtt gtg cga ggt tac tac tta tct gtg ttt ctg gag ctc 192
 Gly Asn Gly Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu
 50 55 60

tca gct ggc ttg cct gaa act tct aaa tat gaa tat cgt gta gag atg 240
 Ser Ala Gly Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met
 65 70 75 80

gtt cac cag tcc tgt aat gat cct aca aaa aat atc att cga gaa ttt 288

Val His Gln Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe
85 90 95

gca tct gac ttt gaa gtt gga gaa tgc tgg ggc tat aat aga ttt ttc 336
Ala Ser Asp Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe
100 105 110

cgt ttg gac tta ctc gca aat gaa gga tac ttg aat cca caa aat gat 384
Arg Leu Asp Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp
115 120 125

aca gtg att tta agg ttt cag gta cgt tca cca act ttc ttt caa aaa 432
Thr Val Ile Leu Arg Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys
130 135 140

tcc cgg gac cag cat tgg tac att act 459
Ser Arg Asp Gln His Trp Tyr Ile Thr
145 150

<210> 12

<211> 153

<212> PRT

<213> Homo sapiens

<400> 12

Phe Thr Ser Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu
1 5 10 15

Glu Asn Phe Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro
20 25 30

Pro Leu Gln Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp
35 40 45

Gly Asn Gly Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu
50 55 60

Ser Ala Gly Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met
65 70 75 80

Val His Gln Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe
85 90 95

Ala Ser Asp Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe
100 105 110

Arg Leu Asp Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp

115

120

125

Thr Val Ile Leu Arg Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys
 130 135 140

Ser Arg Asp Gln His Trp Tyr Ile Thr
 145 150

<210> 13

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

gcgaattcca ggccgcg

17

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

ttcctcgagc cgacttagcc tgtgtgc

27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

cttcgaattc gcgatgtcaa gggttcc

27

<210> 16

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

ccatgctcga ggtattctag ccagaaatg

29

<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

ccagaattca ccagtgaatt agtgcc

26

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

ccactcgagt aatgtaccaa tgctagtcc

29

<210> 19

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
Sequence

<220>

<221> SITE

<222> (2)..(22)

<223> Xaa = any amino acid

<220>

<221> UNSURE
<222> (19)..(22)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (24)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (26)..(28)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (30)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (32)..(47)
<223> Xaa=any amino acid

<220>
<221> UNSURE
<222> (47)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (49)..(76)
<223> Xaa=any amino acid

<220>
<221> UNSURE
<222> (73)..(76)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (78)..(93)
<223> Xaa=any amino acid

<220>
<221> UNSURE
<222> (93)
<223> Xaa may or may not be present

<400> 19

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa

65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp

85 90

<210> 20

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (2)

<223> Xaa =any amino acid

<220>

<221> SITE

<222> (4)

<223> Xaa=any amino acid

<220>

<221> SITE

<222> (5)

<223> Xaa =Leu or Ile

<220>

<221> SITE

<222> (6)

<223> Xaa =any amino acid

<220>

<221> SITE

<222> (8)
<223> Xaa = any amino acid

<220>
<223> Description of Artificial Sequence: Consensus
Sequence

<400> 20
Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro
1 5

<210> 21.
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (2)..(14)
<223> Xaa=any amino acid

<220>
<221> UNSURE
<222> (12)..(14)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (16)..(22)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (26)..(28)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (32)..(42)
<223> Xaa = any amino acid

<220>
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<222> (42)
<223> Xaa may or may not be present

<220>

<221> SITE
 <222> (44)..(47)
 <223> Xaa = any amino acid

 <220>
 <221> UNSURE
 <222> (73)..(76)
 <223> Xaa may or may not be present

<220>
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 <222> (78)..(87)
 <223> Xaa = any amino acid

<220>
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 <222> (87)
 <223> Xaa may or may not be present

<220>
 <221> SITE
 <222> (89)..(93)
 <223> Xaa=any amino acid

<220>
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 <222> (96)..(98)
 <223> Xaa=any amino acid

<220>
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 <222> (100)..(115)
 <223> Xaa=any amino acid

<220>
 <221> SITE
 <222> (117)..(123)
 <223> Xaa=any amino acid

<220>
 <221> UNSURE
 <222> (122)..(123)
 <223> Xaa may or may not be present

<220>
 <223> Description of Artificial Sequence: Consensus
 Sequence

<220>
 <221> UNSURE
 <222> (22)
 <223> Xaa may or may not be present

<220>
 <221> SITE
 <222> (24)
 <223> Xaa=any amino acid

<220>
 <221> SITE
 <222> (30)
 <223> Xaa=any amino acid

<220>
 <221> SITE
 <222> (49)..(76)
 <223> Xaa = any amino acid

<400> 21
 Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Trp Gly Xaa
 85 90 95
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110
 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
 115 120

<210> 22
 <211> 124

<212> PRT
<213> Artificial Sequence

<220>
<221> SITE
<222> (2)..(5)
<223> Xaa =any amino acid

<220>
<221> SITE
<222> (6)
<223> Xaa = Val, Leu, or Ile

<220>
<221> SITE
<222> (7)..(14)
<223> Xaa =any amino acid

<220>
<221> SITE
<222> (16)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (17)
<223> Xaa = Pro or Gly

<220>
<221> SITE
<222> (18)..(22)
<223> Xaa =any amino acid

<220>
<221> UNSURE
<222> (22)..(22)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (24)
<223> Xaa =any amino acid

<220>
<221> SITE
<222> (26)
<223> Xaa =any amino acid

<220>
<221> SITE
<222> (27)
<223> Xaa =Val, Leu or Ile

<220>
<221> SITE
<222> (28)
<223> Xaa = any amino acid

<220>
<221> SITE
<222> (30)
<223> Xaa = any amino acid

<220>
<221> SITE
<222> (32)..(42)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (42)..(42)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (44)
<223> Xaa =Val, Leu or Ile

<220>
<221> SITE
<222> (45)..(47)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (49)..(66)
<223> Xaa=any amino acid

<220>
<221> UNSURE
<222> (65)..(66)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (67)

<223> Xaa=Val, Leu or Ile

<220>

<221> SITE

<222> (68)..(73)

<223> Xaa = any amino acid

<220>

<221> SITE

<222> (74)

<223> Xaa=Asp, Glu, Asn or Gln

<220>

<221> SITE

<222> (75)..(76)

<223> Xaa = any amino acid

<220>

<223> Description of Artificial Sequence: Consensus
Sequence

<220>

<221> UNSURE

<222> (13)..(14)

<223> Xaa may or may not be present

<220>

<221> UNSURE

<222> (72)..(73)

<223> Xaa may or may not be present

<220>

<221> SITE

<222> (78)..(87)

<223> Xaa = any amino acid

<220>

<221> UNSURE

<222> (87)

<223> Xaa may or may not be present

<220>

<221> SITE

<222> (89)..(93)

<223> Xaa=any amino acid

<220>

<221> SITE

<222> (96)
<223> Xaa=Trp or Phe

<220>
<221> SITE
<222> (97)..(98)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (100)..(104)
<223> Xaa = any amino acid

<220>
<221> SITE
<222> (105)
<223> Xaa=Val, Leu or Ile

<220>
<221> SITE
<222> (106)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (107)
<223> Xaa=Asp, Glu, Asn or Gln

<220>
<221> SITE
<222> (108)..(114)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (115)
<223> Xaa=Asp, Glu, Asn or Gln

<220>
<221> SITE
<222> (117)
<223> Xaa=any amino acid

<220>
<221> SITE
<222> (118)
<223> Xaa=Val, Leu or Ile

<220>
<221> SITE
<222> (119)..(122)
<223> Xaa=any amino acid

<220>
~~<221> UNSURE~~
<222> (121)..(122)
<223> Xaa may or may not be present

<220>
<221> SITE
<222> (123)
<223> Xaa=Asp, Glu, Asn or Gln

<400> 22
Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Trp Xaa Xaa Xaa Val Xaa Pro Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Leu
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Trp Gly Xaa
85 90 95

Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
115 120

<210> 23
<211> 139
<212> PRT
<213> Homo sapiens

<400> 23
Asp Met Glu Asp Asp Thr Ser Trp Arg Ser Glu Ala Thr Phe Gln Phe

1	5	10	15
Thr Val Glu Arg Phe Ser Arg Leu Ser Glu Ser Val Leu Ser Pro Pro			
20	25	30	
Cys Phe Val Arg Asn Leu Pro Trp Lys Ile Met Val Met Pro Arg Phe			
35	40	45	
Tyr Pro Asp Arg Pro His Gln Lys Ser Val Gly Phe Phe Leu Gln Cys			
50	55	60	
Asn Ala Glu Ser Asp Ser Thr Ser Trp Ser Cys His Ala Gln Ala Val			
65	70	75	80
Leu Lys Ile Ile Asn Tyr Arg Asp Asp Glu Lys Ser Phe Ser Arg Arg			
85	90	95	
Ile Ser His Leu Phe Phe His Lys Glu Asn Asp Trp Gly Phe Ser Asn			
100	105	110	
Phe Met Ala Trp Ser Glu Val Thr Asp Pro Glu Lys Gly Phe Ile Asp			
115	120	125	
Asp Asp Lys Val Thr Phe Glu Val Phe Val Gln			
130	135		
<210> 24			
<211> 132			
<212> PRT			
<213> Homo sapiens			
<400> 24			
Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met			
1	5	10	15
Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys			
20	25	30	
Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser			
35	40	45	
Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser			
50	55	60	
Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu			
65	70	75	80

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
85 90 95

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
100 105 110

~~Glu-Ala-Asn-Gly-Leu-Leu-Pro-Asp-Asp-Lys-Leu-Thr-Leu-Phe-Cys-Glu~~
115 120 125

Val Ser Val Val
130

<210> 25

<211> 135

<212> PRT

<213> Homo sapiens

<400> 25

Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe
1 5 10 15

Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln
20 25 30

Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly
35 40 45

Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly
50 55 60

Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln
65 70 75 80

Ser Cys Asn Asp Pro Thr Lys Asn Ile Ile Arg Glu Phe Ala Ser Asp
85 90 95

Phe Glu Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp
100 105 110

Leu Leu Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile
115 120 125

Leu Arg Phe Gln Val Arg Ser
130 135

<210> 26

<211> 150
 <212> PRT
 <213> Homo sapiens

<400> 26

Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr Arg Arg Cys His Glu
 1 5 10 15

Ser Ala Cys Gly Arg Thr Val Ser Leu Phe Ser Pro Ala Phe Tyr Thr
 20 25 30

Ala Lys Tyr Gly Tyr Lys Leu Cys Leu Arg Leu Tyr Leu Asn Gly Asp
 35 40 45

Gly Thr Gly Lys Arg Thr His Leu Ser Leu Phe Ile Val Ile Met Arg
 50 55 60

Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Arg Asn Lys Val Thr
 65 70 75 80

Phe Met Leu Leu Asp Gln Asn Asn Arg Glu His Ala Ile Asp Ala Phe
 85 90 95

Arg Pro Asp Leu Ser Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr
 100 105 110

Asn Val Ala Ser Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln
 115 120 125

Ser Pro Lys His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys
 130 135 140

Ile Val Glu Thr Ser Thr
 145 150

<210> 27
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 27

Gly Val Phe Ile Trp Lys Ile Ser Asp Phe Ala Arg Lys Arg Gln Glu
 1 5 10 15

Ala Val Ala Gly Arg Ile Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr
 20 25 30

Ser Arg Tyr Gly Tyr Lys Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp
35 40 45

Gly Thr Gly Arg Gly Thr His Leu Ser Leu Phe Phe Val Val Met Lys
50 55 60

Gly Pro Asn Asp Ala Leu Leu Arg Trp Pro Phe Asn Gln Lys Val Thr
65 70 75 80

Leu Met Leu Leu Asp Gln Asn Asn Arg Glu His Val Ile Asp Ala Phe
85 90 95

Arg Pro Asp Val Thr Ser Ser Ser Phe Gln Arg Pro Val Asn Asp Met
100 105 110

Asn Ile Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu
115 120 125

Ala Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile
130 135 140

Val Asp Leu Thr Gly Leu
145 150

<210> 28

<211> 153

<212> PRT

<213> Homo sapiens

<400> 28

Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu
1 5 10 15

Ala Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr
20 25 30

Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp
35 40 45

Gly Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg
50 55 60

Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr
65 70 75 80

Leu Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala
85 90 95

Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Ile Gly Glu
100 105 110

Met Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu
115 120 125

Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile
130 135 140

Val Asp Thr Ser Asp Leu Pro Asp Pro
145 150

<210> 29

<211> 163

<212> PRT

<213> Homo sapiens

<400> 29

Gly Val Leu Ile Trp Lys Ile Gly Ser Tyr Gly Arg Arg Leu Gln Glu
1 5 10 15

Ala Lys Ala Lys Pro Asn Leu Glu Cys Phe Ser Pro Ala Phe Tyr Thr
20 25 30

His Lys Tyr Gly Tyr Lys Leu Gln Val Ser Ala Phe Leu Asn Gly Asn
35 40 45

Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg Val Leu Pro
50 55 60

Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg Arg Val Thr
65 70 75 80

Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys Pro Gln His
85 90 95

Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn Phe Gln Lys
100 105 110

Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu Gly Phe Gly
115 120 125

Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg Asn Tyr Val
130 135 140

Arg Asp Asp Ala Val Phe Ile Arg Ala Ala Val Glu Leu Pro Arg Lys

145

150

155

160

Ile Leu Ser

<210> 30

<211> 154

<212> PRT

<213> Homo sapiens

<400> 30

Gly Lys Leu Ile Trp Lys Val Thr Asp Tyr Lys Met Lys Lys Arg Glu
 1 5 10 15

Ala Val Asp Gly His Thr Val Ser Ile Phe Ser Gln Ser Phe Tyr Thr
 20 25 30

Ser Arg Cys Gly Tyr Arg Leu Cys Ala Arg Ala Tyr Leu Asn Gly Asp
 35 40 45

Gly Ser Gly Arg Gly Ser His Leu Ser Leu Tyr Phe Val Val Met Arg
 50 55 60

Gly Glu Phe Asp Ser Leu Leu Gln Trp Pro Phe Arg Gln Arg Val Thr
 65 70 75 80

Leu Met Leu Leu Asp Gln Ser Gly Lys Lys Asn Ile Met Glu Thr Phe
 85 90 95

Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Arg Pro Asp Gly Glu Met
 100 105 110

Asn Ile Ala Ser Gly Cys Pro Arg Phe Val Ala His Ser Val Leu Glu
 115 120 125

Asn Ala Lys Asn Ala Tyr Ile Lys Asp Asp Thr Leu Phe Leu Lys Val
 130 135 140

Ala Val Asp Leu Thr Asp Leu Glu Asp Leu
 145 150

<210> 31

<211> 157

<212> PRT

<213> Homo sapiens

<400> 31

Gly Ile Tyr Ile Trp Lys Ile Gly Asn Phe Gly Met His Leu Lys Cys
1 5 10 15

Gln Glu Glu Glu Lys Pro Val Val Ile His Ser Pro Gly Phe Tyr Thr
20 25 30

Gly Lys Pro Gly Tyr Lys Leu Cys Met Arg Leu His Leu Gln Leu Pro
35 40 45

Thr Ala Gln Arg Cys Ala Asn Tyr Ile Ser Leu Phe Val His Thr Met
50 55 60

Gln Gly Glu Tyr Asp Ser His Leu Pro Trp Pro Phe Gln Gly Thr Ile
65 70 75 80

Arg Leu Thr Ile Leu Asp Gln Ser Glu Ala Pro Val Arg Gln Asn His
85 90 95

Glu Glu Ile Met Asp Ala Lys Pro Glu Leu Leu Ala Phe Gln Arg Pro
100 105 110

Thr Ile Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val Thr Phe Met His
115 120 125

Leu Glu Ala Leu Arg Gln Arg Thr Phe Ile Lys Asp Asp Thr Leu Leu
130 135 140

Val Arg Cys Glu Val Ser Thr Arg Phe Asp Met Gly Ser
145 150 155

<210> 32

<211> 964

<212> PRT

<213> Homo sapiens

<400> 32

Met Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val Phe Arg Cys Phe
1 5 10 15

Ile Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys Pro His Cys Ser
20 25 30

Lys Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu Thr Glu Gln Arg
35 40 45

Ala Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu Arg Glu Leu Val

50

55

60

Asn Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu Asp Thr Leu Gln
65 70 75 80

Leu Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys Asp Lys Cys Glu
85 90 95

Asn His His Glu Lys Leu Ser Val Phe Cys Trp Thr Cys Lys Lys Cys
100 105 110

Ile Cys His Gln Cys Ala Leu Trp Gly Gly Met His Gly Gly His Thr
115 120 125

Phe Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val Thr Lys Val Asn
130 135 140

Glu Glu Val Ala Lys Leu Arg Arg Arg Leu Met Glu Leu Ile Ser Leu
145 150 155 160

Val Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg Asn Ala Lys Asp
165 170 175

Glu Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met Met Ile Ala Arg
180 185 190

Leu Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu Met Gly Gln Lys
195 200 205

Thr Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser Leu Leu Gln Glu
210 215 220

Val Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu Leu Ile Ser Lys
225 230 235 240

Ser Ser Glu Ile Leu Met Met Phe Gln Gln Val His Arg Lys Pro Met
245 250 255

Ala Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe Thr Ser Glu Leu
260 265 270

Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu Asn Phe Ser Thr
275 280 285

Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro Leu Gln Val Ser
290 295 300

Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly Asn Gly Val Val

305 310 315 320
 Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser Ala Gly Leu Pro
 325 330 335
 Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val His Gln Ser Cys
 340 345 350
 Asn Asp Pro Thr Lys Asn Ile Ile Arg Cys Phe Ala Ser Asp Phe Glu
 355 360 365
 Val Gly Glu Cys Trp Gly Tyr Asn Arg Phe Phe Arg Leu Asp Leu Leu
 370 375 380
 Ala Asn Glu Gly Tyr Leu Asn Pro Gln Asn Asp Thr Val Ile Leu Arg
 385 390 395 400
 Phe Gln Val Arg Ser Pro Thr Phe Phe Gln Lys Ser Arg Asp Gln His
 405 410 415
 Trp Tyr Thr Ile Gln Leu Glu Ala Ala Gln Thr Ser Tyr Ile Gln Gln
 420 425 430
 Ile Asn Asn Leu Lys Glu Arg Leu Thr Ile Glu Leu Ser Arg Thr Gln
 435 440 445
 Lys Ser Arg Asp Leu Ser Pro Pro Asp Asn His Leu Ser Pro Gln Asn
 450 455 460
 Asp Asp Ala Leu Glu Thr Arg Ala Lys Lys Ser Ala Cys Ser Asp Met
 465 470 475 480
 Leu Leu Glu Gly Gly Pro Thr Thr Ala Ser Val Arg Glu Ala Lys Glu
 485 490 495
 Asp Glu Glu Asp Glu Glu Lys Ile Gln Asn Glu Asp Tyr His His Glu
 500 505 510
 Leu Ser Asp Gly Asp Leu Asp Leu Asp Leu Val Tyr Glu Asp Glu Val
 515 520 525
 Asn Gln Leu Asp Gly Ser Ser Ser Ser Ala Ser Ser Thr Ala Thr Ser
 530 535 540
 Asn Thr Glu Glu Asn Asp Ile Asp Glu Glu Thr Met Ser Gly Glu Asn
 545 550 555 560
 Asp Val Glu Tyr Asn Asn Met Glu Leu Glu Glu Gly Glu Leu Met Glu

565

570

575

Asp Ala Ala Ala Ala Gly Pro Ala Gly Ser Ser His Gly Tyr Val Gly
580 585 590

Ser Ser Ser Arg Ile Ser Arg Arg Thr His Leu Cys Ser Ala Ala Thr
595 600 605

Ser Ser Leu Leu Asp Ile Asp Pro Leu Ile Leu Ile His Leu Leu Asp
610 615 620

Leu Lys Asp Arg Ser Ser Ile Glu Asn Leu Trp Gly Leu Gln Pro Arg
625 630 635 640

Pro Pro Ala Ser Leu Leu Gln Pro Thr Ala Ser Tyr Ser Arg Lys Asp
645 650 655

Lys Asp Gln Arg Lys Gln Gln Ala Met Trp Arg Val Pro Ser Asp Leu
660 665 670

Lys Met Leu Lys Arg Leu Lys Thr Gln Met Ala Glu Val Arg Cys Met
675 680 685

Lys Thr Asp Val Lys Asn Thr Leu Ser Glu Ile Lys Ser Ser Ser Ala
690 695 700

Ala Ser Gly Asp Met Gln Thr Ser Leu Phe Ser Ala Asp Gln Ala Ala
705 710 715 720

Leu Ala Ala Cys Gly Thr Glu Asn Ser Gly Arg Leu Gln Asp Leu Gly
725 730 735

Met Glu Leu Leu Ala Lys Ser Ser Val Ala Asn Cys Tyr Ile Arg Asn
740 745 750

Ser Thr Asn Lys Lys Ser Asn Ser Pro Lys Pro Ala Arg Ser Ser Val
755 760 765

Ala Gly Ser Leu Ser Leu Arg Arg Ala Val Asp Pro Gly Glu Asn Ser
770 775 780

Arg Ser Lys Gly Asp Cys Gln Thr Leu Ser Glu Gly Ser Pro Gly Ser
785 790 795 800

Ser Gln Ser Gly Ser Arg His Ser Ser Pro Arg Ala Leu Ile His Gly
805 810 815

Ser Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg Gln Cys Lys Ala

820

825

830

Leu Asp Ser Asp Ala Val Val Val Ala Val Phe Ser Gly Leu Pro Ala
835 840 845

Val Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala Asn Ala Lys Gly
850 855 860

Gly His Leu Phe Gly Leu Gln Met Thr Asp Leu Glu Asn Asn Ser Glu
865 870 875 880

Thr Gly Phe Leu Gln Pro Val Leu Pro Glu Gly Ala Ser Ala Ala Pro
885 890 895

Glu Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Gly Asp Thr Glu Asn
900 905 910

Glu Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe His Asp Ser Phe
915 920 925

Met Val Met Thr Gln Pro Pro Asp Glu Asp Thr His Ser Ser Glu Pro
930 935 940

Asp Gly Phe Gln Ile Gly Pro Glu Asp Leu Ser Phe Asn Thr Asp Glu
945 950 955 960

Asn Ser Gly Arg